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     3 <110> APPLICANT: EXELIXIS, INC.
     5 <120> TITLE OF INVENTION: ANIMAL MODELS AND METHODS FOR ANALYSIS OF LIPID METABOLISM
AND SCREENING
     6       OF PHARMACEUTICAL AND PESTICIDAL AGENTS THAT MODULATE LIPID METABOLISM
     8 <130> FILE REFERENCE: EX99-004C-US
    10 <140> CURRENT APPLICATION NUMBER: 10/018,248A
C--> 11 <141> CURRENT FILING DATE: 2002-07-30
    13 <150> PRIOR APPLICATION NUMBER: US 60/189,700
    14 <151> PRIOR FILING DATE: 2000-03-15
    16 <150> PRIOR APPLICATION NUMBER: US 09/332,522
    17 <151> PRIOR FILING DATE: 1999-06-14
    19 <160> NUMBER OF SEQ ID NOS: 8
    21 <170> SOFTWARE: PatentIn version 3.1
    23 <210> SEQ ID NO: 1
    24 <211> LENGTH: 3419
    25 <212> TYPE: DNA
    26 <213> ORGANISM: Caenorhabditis elegans
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    33 cgctcgattt tgacatggag cacaactggc aagagcccgg accatcacaa caaccggatc     180
    35 catcaattcc cggaaatcaa cacagtccgc cacaggaata ttatgatatt gatggtcaac     240
    37 gagacgtaag caccttacac tccctgctca accacaacaa cgacgacttc ttctcaatgc     300
    39 gattttcccc gccaaacttt gatctcggcg gaggccgtgg accttctcta gccgccaccc     360
    41 aacaattatc tggagaaggt cctgcaagta tgcttaaccc cttacaaaca tctccaccaa     420
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    45 cgccagcgat gactccacat caggcagcgt cgcttttgt taatactaat ggaattgatc     540
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    49 catatacaga agccatggga catatcaacg ggtacatgtc tccatacgac caagctcaag     660
    51 gcccatcagg accatcatat tactcacaac accatcaatc tccaccacct catcaccacc     720
    53 atcaccaccc gatgccaaaa atccatgaga accctgaaca agtggcatct ccatcgattg     780
    55 aagatgctcc agagacgaaa ccaactcatt tggttgaacc acaaagtcca aaaagcccgc     840
    57 agaatatgaa agaggagctt cttcggttac tagttaacat gtctccgagt gaagttgaac     900
    59 ggttaaagaa taaaaaatca ggagcatgtt cagcgacgaa tgggccatcg aggagtaagg     960
    61 agaaggcggc gaagattgtg attcaggaga cagcggaagg ggatgaagat gaggatgatg    1020
    63 aggatagtga ttccggggag actatgtctc agggaactac tattattgtt cgaagaccaa    1080
    65 aaaccgagcg tcgtacggca cacaatctca tcgaaaagaa gtatagatgc tcaataaatg    1140
    67 atcgaattca acagctgaaa gtactttgt gtggggatga agctaagctt tcaaaatcgg    1200
    69 caacactacg acgggctatt gaacatatcg aggaggttga acacgagaat caggtgttga    1260
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Input Set : **A:\10018248a.raw.txt**
Output Set: **N:\CRF4\02112003\J018248A.raw**

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 85 tatatgtggt tgtcaaactg ctgatccatg gtgaccctgt tcaagacttc atgtccgttt   1740
 87 catggcagac ttttgtgacg actcgagaga aggcgagagc cgagttgaac tctggaaatt   1800
 89 tgaaagatgc tcagagaaag ttctgcgagt gtcttgcaac gttggatcga tcgcttccat   1860
 91 caccgggggt tgattcggtg ttttcggttg ctgggaatg cgttcgacat cttttgaatt    1920
 93 ggttgtggat cgggagatac atcgcaagaa ggcgcaggtc caccacgaag cctgtctcag   1980
 95 tcgtttgtag gagtcatgcg cagactgcag ttctctatca tgaaattcat cagctccatc   2040
 97 taatgggtat cactggaaac ttcgaagaca cctatgaacc atccgcccta acgggcctct   2100
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113 caaaaaatgt ggaacgcatc ctaaatgaca atgaccgtct cgatgatgaa gtagacgtgg   2580
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117 agaaggatga gtcagcgaaa ttcggaacct ggatctctcg aaacggagat gcttgttgca   2700
119 catggtggac gcacgttctg acatgtggaa tctattggag gagtaacaag aatgagctgg   2760
121 cacggcaaca ctattcactg atcaggaact gtccgccgaa gatttttgaca gacaatctgg   2820
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129 tggcctacga atggattatg aactcgctgc tcgacgcgtg gcgttccaat ctattcgcat   3060
131 cgaaacccta ctggacacaa agcttcaagg gacaatccac gtttagtacg ctttatcaag   3120
133 aggcgtataa tcattatgcg attattaatg ggacaagggg agattgttgg agactatttg   3180
135 tctacgagct cacgtgccga atgctcaacg gagccaaccc acaagccacg tggtcaggcg   3240
137 yccgacgcgt tcgatctaca aaaatggacg cggtccgagg aagagtgagc atgcgacgct   3300
139 cggctcaacc ggacgcattt catcttcata cactggttaa actacatact tctatggatc   3360
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146 <212> TYPE: PRT
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152 <223> OTHER INFORMATION: "X" is any amino acid
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162             20                  25                  30
165 Pro Leu Asp Phe Asp Met Glu His Asn Trp Gln Glu Pro Gly Pro Ser
166         35                  40                  45
169 Gln Gln Pro Asp Pro Ser Ile Pro Gly Asn Gln His Ser Pro Pro Gln
170     50                  55                  60
173 Glu Tyr Tyr Asp Ile Asp Gly Gln Arg Asp Val Ser Thr Leu His Ser
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Input Set : **A:\10018248a.raw.txt**
Output Set: **N:\CRF4\02112003\J018248A.raw**

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178               85                   90                   95
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182               100                 105                 110
185 Gln Gln Leu Ser Gly Glu Gly Pro Ala Ser Met Leu Asn Pro Leu Gln
186          115                 120                 125
189 Thr Ser Pro Pro Ser Gly Gly Tyr Pro Pro Ala Asp Ala Tyr Arg Pro
190       130                 135                 140
193 Leu Ser Leu Ala Gln Gln Leu Ala Ala Pro Ala Met Thr Pro His Gln
194 145                 150                 155                 160
197 Ala Ala Ser Leu Phe Val Asn Thr Asn Gly Ile Asp Gln Lys Asn Phe
198               165                 170                 175
201 Thr His Ala Met Leu Ser Ser Pro His His Thr Ser Met Thr Ser Gln
202          180                 185                 190
205 Pro Tyr Thr Glu Ala Met Gly His Ile Asn Gly Tyr Met Ser Pro Tyr
206          195                 200                 205
209 Asp Gln Ala Gln Gly Pro Ser Gly Pro Ser Tyr Tyr Ser Gln His His
210       210                 215                 220
213 Gln Ser Pro Pro Pro His His His His His His Pro Met Pro Lys Ile
214 225                 230                 235                 240
217 His Glu Asn Pro Glu Gln Val Ala Ser Pro Ser Ile Glu Asp Ala Pro
218               245                 250                 255
221 Glu Thr Lys Pro Thr His Leu Val Glu Pro Gln Ser Pro Lys Ser Pro
222          260                 265                 270
225 Gln Asn Met Lys Glu Glu Leu Leu Arg Leu Leu Val Asn Met Ser Pro
226          275                 280                 285
229 Ser Glu Val Glu Arg Leu Lys Asn Lys Lys Ser Gly Ala Cys Ser Ala
230       290                 295                 300
233 Thr Asn Gly Pro Ser Arg Ser Lys Glu Lys Ala Ala Lys Ile Val Ile
234 305                 310                 315                 320
237 Gln Glu Thr Ala Glu Gly Asp Glu Asp Glu Asp Asp Glu Asp Ser Asp
238               325                 330                 335
241 Ser Gly Glu Thr Met Ser Gln Gly Thr Thr Ile Ile Val Arg Arg Pro
242          340                 345                 350
245 Lys Thr Glu Arg Arg Thr Ala His Asn Leu Ile Glu Lys Lys Tyr Arg
246          355                 360                 365
249 Cys Ser Ile Asn Asp Arg Ile Gln Gln Leu Lys Val Leu Leu Cys Gly
250       370                 375                 380
253 Asp Glu Ala Lys Leu Ser Lys Ser Ala Thr Leu Arg Arg Ala Ile Glu
254 385                 390                 395                 400
257 His Ile Glu Glu Val Glu His Glu Asn Gln Val Leu Lys His His Val
258               405                 410                 415
261 Glu Gln Met Arg Lys Thr Leu Gln Asn Asn Arg Leu Pro Tyr Pro Glu
262          420                 425                 430
265 Pro Ile Gln Tyr Thr Glu Tyr Ser Ala Arg Ser Pro Val Glu Ser Ser
266          435                 440                 445
269 Pro Ser Pro Pro Arg Asn Glu Arg Lys Arg Ser Arg Met Ser Thr Thr
270       450                 455                 460
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273 Thr Pro Met Lys Asn Gly Thr Arg Asp Gly Ser Ser Lys Val Thr Leu
274 465             470             475                     480
277 Phe Ala Met Leu Leu Ala Val Leu Ile Phe Asn Pro Ile Gly Leu Leu
278             485             490                 495
281 Ala Gly Ser Ala Ile Phe Ser Lys Ala Ala Ala Glu Ala Pro Ile Ala
282             500             505                 510
285 Ser Pro Phe Glu His Gly Arg Val Ile Asp Asp Pro Asp Gly Thr Ser
286         515             520             525
289 Thr Arg Thr Leu Phe Trp Glu Gly Ser Ile Ile Asn Met Ser Tyr Val
290     530             535             540
293 Trp Val Phe Asn Ile Leu Met Ile Ile Tyr Val Val Val Lys Leu Leu
294 545             550             555                     560
297 Ile His Gly Asp Pro Val Gln Asp Phe Met Ser Val Ser Trp Gln Thr
298             565             570                 575
301 Phe Val Thr Thr Arg Glu Lys Ala Arg Ala Glu Leu Asn Ser Gly Asn
302             580             585                 590
305 Leu Lys Asp Ala Gln Arg Lys Phe Cys Glu Cys Leu Ala Thr Leu Asp
306         595             600             605
309 Arg Ser Leu Pro Ser Pro Gly Val Asp Ser Val Phe Ser Val Gly Trp
310     610             615             620
313 Glu Cys Val Arg His Leu Leu Asn Trp Leu Trp Ile Gly Arg Tyr Ile
314 625             630             635                     640
317 Ala Arg Arg Arg Arg Ser Thr Thr Lys Pro Val Ser Val Val Cys Arg
318             645             650                 655
321 Ser His Ala Gln Thr Ala Val Leu Tyr His Glu Ile His Gln Leu His
322             660             665                 670
325 Leu Met Gly Ile Thr Gly Asn Phe Glu Asp Thr Tyr Glu Pro Ser Ala
326         675             680             685
329 Leu Thr Gly Leu Phe Met Ser Leu Cys Ala Val Asn Leu Ala Glu Ala
330     690             695             700
333 Ala Gly Ala Ser Asn Asp Gly Leu Pro Arg Ala Val Met Ala Gln Ile
334 705             710             715                     720
337 Tyr Ile Ser Ala Ser Ile Gln Cys Arg Leu Ala Leu Pro Asn Leu Leu
338             725             730                 735
341 Ala Pro Phe Phe Ser Gly Tyr Phe Leu Arg Arg Ala Arg Arg His Val
342         740             745             750
345 Arg Arg Ala Pro Glu His Ser Val Ser His Leu Leu Trp Ile Phe His
346         755             760             765
349 Pro Ala Thr Arg Lys Phe Met Ser Asp Ala Lys Arg Leu Glu His Val
350     770             775             780
353 Leu Ser Ser Lys Gln Lys Gln Leu Arg Phe Gly Ser Phe Val Glu Asp
354 785             790             795                     800
357 Glu Gln Leu Ser Pro Leu Ala Arg Ile Arg Thr Thr Leu Lys Val Tyr
358             805             810                 815
361 Leu Leu Ser Lys Leu Val Gln Glu Leu Val Gly Gly Asp Glu Ile Phe
362             820             825                 830
365 Thr Lys Asn Val Glu Arg Ile Leu Asn Asp Asn Asp Arg Leu Asp Asp
366         835             840             845
369 Glu Val Asp Val Val Asp Val Ser Arg Leu Leu Val Thr Ile Ser Thr
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377 Gly Thr Trp Ile Ser Arg Asn Gly Asp Ala Cys Cys Thr Trp Trp Thr
378                 885                 890                 895
381 His Val Leu Thr Cys Gly Ile Tyr Trp Arg Ser Asn Lys Asn Glu Leu
382                 900                 905                 910
385 Ala Arg Gln His Tyr Ser Leu Ile Arg Asn Cys Pro Pro Lys Ile Leu
386             915                 920                 925
389 Thr Asp Asn Leu Gly Leu Ala Val Gly His Ala Leu Cys Ala Arg Lys
390             930                 935                 940
393 Ile Cys Ile Asp Asp Arg Asp Ser Pro Lys Val Ser Gln Tyr Val Cys
394 945                 950                 955                 960
397 Ile His Thr Lys Lys Ser Leu Glu Ser Leu Arg Leu Phe Ser Thr Ser
398                 965                 970                 975
401 Ser Arg Ala Ser Gly Val Val Ser Gly Ile Gln Glu Gly Thr Arg Arg
402             980                 985                 990
405 Met Ala Tyr Glu Trp Ile Met Asn  Ser Leu Leu Asp Ala  Trp Arg Ser
406             995                1000                1005
409 Asn Leu  Phe Ala Ser Lys Pro  Tyr Trp Thr Gln Ser  Phe Lys Gly
410      1010                1015                1020
413 Gln Ser  Thr Phe Ser Thr Leu  Tyr Gln Glu Ala Tyr  Asn His Tyr
414      1025                1030                1035
417 Ala Ile  Ile Asn Gly Thr Arg  Gly Asp Cys Trp Arg  Leu Phe Val
418      1040                1045                1050
421 Tyr Glu  Leu Thr Cys Arg Met  Leu Asn Gly Ala Asn  Pro Gln Ala
422      1055                1060                1065
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426      1070                1075                1080
429 Val Arg  Gly Arg Val Ser Met  Arg Arg Ser Ala Gln  Pro Asp Ala
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447 cgcaagtgac gtccagcaac cggaggaccc ccaactgtag aatccgcatc accatcctaa   180
449 tcccaacaaa ccaatgacat cttgagacct caccagccat ggatcccttc gtgttcttca   240
451 tagtactggc atcgctttat ggcgttcttt acttttтcga ccgcttcttc aagagttgca   300
453 tgcactaccc gtacgatgcc ttcctcaaga acaccgggct gagtataaat ttcatgagcc   360
455 tccactggca cacgagtgcc tttaacagga ccctcctacg ctggggatct gccggtaaca   420
457 gctgcacccg gagagtaatg atcaccagct ttaatgtagg agtcctggtc accttttctc   480
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461 gctcttcgtc tgtatcctcg cccgttggag tccctgtgca gctggaaatt ctactgcccg   600
463 gcgtcaactt gccgttggag gagatcggat actacatcac aacccttgtg ctctgcttgg   660
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Input Set : A:\10018248a.raw.txt
Output Set: N:\CRF4\02112003\J018248A.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 1073
Seq#:7; N Pos. 3038,3049
Seq#:8; Xaa Pos. 993

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5